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AM OI: US-04-525-998A 11 +5 FIE_68 *
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Date: Apr 23, 2002 10:17 PW

About: Results Were produced by the GenCore software, version 4.5, copyright (c) 1993-2000 Compugen Ltd.

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-Modell-frame_intp.model -DEV-xlp
-C.rogn__intsrt__sport_ms^row_fore_pront__states_ltstam_intsrtep_aguery_fasta_1_2007
-DR-DIR_68 -OPMI=Fastan -SUFFIX-Tpr -GAPOP=12.000 -GAPEXT-4.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | MINNATCH | 0.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.0
Command line parameters:
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Search time (sec). 113.890000 Database: PIR_68:* Database sequences: 219241 Database length: 76174552 Search information block: Query: US-09-525-998A-11 Query length: 600

! probable transcription requiate
! furin (EC 3.4.21.75) | fall ax human CX40 homolog Portmentation 8 76-06 1.1e 05 5 56-06 7.3e-07 0.0051 0.0124 0.0164 0.0124 0.0228 0.0233 0.0233 0 0005 0.0003 0.0004 0.0022 0.0028 Strd Orig 75corts 1117 5 00 1550 46 1774 50 1210 14 1774 50 1141 49 1213 50 50 509 57 193 50 500 79 30 143.50 137.50 134.00 11.43 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1 133.00 JCE148 S12783 ::727283 ::A48820 pir2.C42125 pir1:A46517 DRARAR A35356 pir2:J⊆2395 pir1:TN0006 534583 pir2:G02428 137316 T31070 score_list: pirl:GQHUT1 :JC1302 pirl:GUMST1 : A26.431 H43692 pir2:B38634 148854 A46476 A46484 pir1:A49053 AFO77 A43434 148700 137383 :A42086 A40036 :T23433 : A48434 T43251 COVEME NUHCO:

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C. Species: Homo capiens (man)
C. Species: Manual 1992 mergraphs A 4.6ff; A94291. SLOG7, J16758, A60231:
R. Pruchs, P.: Strohl, S.: Deorzak, M. Himmicr, A.: Ambios, P.F.
CCCOMMICS 12, 219-221, 1992
A. Setochard of the human in Proceptor 1 (p60) gene (in PF) and localization to A. Reference commics: A 48208 multiply 2250449
A. Reference commics: A 48208 multiply 2250449
A. Residue: Lype: DNA
A. Residue: 1455 ePho.
A. Residue: 1455 ePho.
A. Cross-references: DNA F864, CM: MATSH65; GM: M75466; Niby 4139748, Phin: Aashallolip Pl
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Cell F., 351-359, 1990
Affilie, Molecular clouing and expression of the human 55 kd tumor necrosis factor re
A;Reference number: A:4899, MOID.50235284
                                               tumor necrosis factor receptor | precursor [validated] | human
NATACLINE LUMOS (FT 1951 NATACLINE factor receptor (MF receptor type )
NYCentains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
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A. Andreas Date, Sider, Mulc.91006011
A. Molecule types mRNA
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A. Notes gaits of solubic THF binding protein is including the amino and carboxyl ends R. Kemper, O.S. Wallach, D.
Gena 134, 209-214, 1993 que 64P protein variela vin tumor necrosis factor receptor (252 antique precursor mouse trophorite vistoire 15 auti CD27 antique precursor rat nerve arrowth factor receptor, nerve arrowth factor receptor, 18-eel activation protein CD49 (10rin (EC 3 4.21 75) 2 - trait nerve growth factor receptor pr merve growth factor receptor pd merve growth factor receptor pd 22 posteric - nabelt fibrica vin 72 pecteto - myxema vinis (stia apoptosis mediating membrane as G2R protein - variola minor vin hypotbotinal protein G2R vari ! notch homolog sea urchin (Ly ! hypothetical protein 20485.12 | ! Expethetical protein YG315A.f apoptosis mediating surface ant Phypothetical protein KOBC7.3 Probable laminin alpha chain tumor necrosis factor receptor tumor necrosis factor receptor transcribility and transcribility factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor gene murine tumour peorosis fac R cell-associated surface molec subtilisin'like proprotein conv sabillisin-like propretalin ochv CX40 antigen precursor - rat CD30 antigen precursor - human tumor necrosis factor redeptor variant specific surface proteserine proteinase (RC 3.4.21. gene ox40 protein mouse FAS soluble protein - buman

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ir2:825647	31.7.7	17.50 172.01 0.5641	0.0641	1.4	213 ockinch sarface protein - P	arface	protein -	-

A; Accession: A34899

A)Molocule type: mRNA A)Residues: 1-455 <1285 A:Cross-references: 01:M5B286; GB:M33480; NID;a339753; PIIN:AAA36753.1; PID;a339754 A)Experimental source: placenta

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Lubor necrosis factor receptor p55 precursor - piq
C.Species. Sus scrofa domestica (domestic pig)
C.Hatte. 29 Nov-1925 Requence_revision DB reb 1926 #text_change 23-Jul-1999
C.Accession. JC4302, PC4093
R.Suter, B.: Pauli, U.
A.P.Lile. Cloning of the cDNA encoding the policine p55 tumor necrosis Lactor receptor.
A.Reference number. JC4302, MUTD:96011845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 PACAGIGGACGGGGACACGIGIGIGGCGCGAAGAAGAACAGIACCGGC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 CACCCTCAAAATAATTCCATTTGCTGTACCAAGTGCCACAAGGAACCTA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 HisproclinAshAshScr:?cCysCysThrLysCysHisCysHisLysGlyThrTy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 euglyAspArgGluLysArgAspSerValCysProGlnGlyLysTyrlle 50
                                                                                                                                                         17 uLeuLeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisL 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGA
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                                           Align seg 1/1 to: GQHUT1 from; 1 to: 455
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A,fitie. Cloning and partial characterization of the promoter for the human p55 tumor nd
A;Reference number. 370758, M310.94085779
A;Aecession: J10758
                                                                                                                                                                                                                                                                                                                                                                             A:Molecule type: protein
A;Rosiduds, 41-43, X7-45-53,X7,55-57 -SEC>
R:Gdianaga, V.: Hamp; C.: Kobr. W.; Cappurcini, F.; Lurci III, J.A.; Jeffes, E.W.B.; Ld
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
                                                                                                                                                                                    Riscakinger, P., Vey, E., Turcatti, G., Wingfield, P., Dayer, J.M.
Bar, J. Immunol. 20, 116-1174, 1990
A.Title: Tumor necrosis factor ichibilior. purification, NH-2 terminal amino acid sequence A.Relerence number: A60231; MUID:90292116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AjExperimental source: cancer patient serum
Riolsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.: Thysell, H.; Grubb, A.; Adelt, G.
Eur. J. Haematol. 42, 270-275, 1989
Ajittle. isolation and characterization of a tumor necrosis factor binding protein from A; Reference number: A60594; MUD:89171156
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E;1-21/D-nai; signal segence #status predicted .SIC
E;22-855/Product; tumon mecroass factor receptor | #status predicted xMAT>
E;30-211/Premain extraceilular #status predicted .EXT
E;41-201/Product: TNF Einding profein | ("umer nerrosis factor alpha inhibitor) #status
E;41-201/Product: TNF Einding profein | ("umer nerrosis factor alpha inhibitor) #status
E;44-82/Domain: NGF receptor repeat homology cNG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Title: Purification and characterization of an inhibitor (soluble tumor necrosis factors)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Two tumor necrosis factor binding proteins putified from human unine Evidence A; Reference number: A35010; MUID:90110215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C)Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Kostducs; 41 45 <8MO>
A;Kszputiwental source; normal urine
A;Exportmental source; normal urine
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol Riochem 68, 2266, 2368, 1994
A;Tille: Amino acid sequence of natural tumor necrosis factor alpha inhibitor parifical
A;Reterence number: JC2404; MUID:95128033
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Analg postition: 12613.2-12014.2
A:Introns: 1373: 65/1: 108/1: 188/1: 184/2: 209/1: 247/1: 256/3: 353/1
C.Superfamily: Lamba metrosis factor receptor 15pr 1: NSE receptor repeat homotosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig13-234/Domain, transmembrane *Status predicted AMEMS Fig35-454/Domain, intracellular *status predicted CINTS Fig7Pinding Sites carbohydrate (ASE) (covalent) *status predicted
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A;Rosiduos: 41-53,'X' 55-144,'Y',146-150,'X',152-186,'X',188-201 -KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 94 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Molecule type: protein
A)Residues: 41-43,'X',45-53,'V',55-57,'XK',67 71,7
A)Experimental source; renal tailure patient urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A38258; MUID: 91062364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol Chem 265, 1531-1536, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouality: 1117.50
Ratio: 5.588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 41-60 <GAT>
                                                                                                                                                     A; Residues: 1-13 <KEM>
                                                                                                                 A: Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A60594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AjArression - A38258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Accession: JC2404
                                                                                                                                                                                                                                                                                                                                             A; Accession: A60231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Accession: A35010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;84-126/Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aliqnment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tients.
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A; Molecule type: protein A; Residues: 1-7 <SU2>

alignment_block: US-09-525-998A-11 x SCHUT1

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C.Superfamily, tumor nectors factor receptor type 1, NGF receptor repeat homology C.Keywords: glycoprotein, kidney, receptor, transmembrane protein; tumor E.1-29/Demain: Signal sequence islatus predicted SIG. 830.461/Product: tumor necrosis predicted SIG. 8130.461/Product: tumor necrosis predicted FS #status predicted CMATS E.44-194/Promain: extraoralitation rich #status predicted CMATS E.44-194/Demain: After treether repeat homology NGS.
                                                                                                                                                                                                                                                                                                      F:84-126/Dominin: NGF reciptor Topost humology NNFF

F:21 231/Operain: Transminhrane #strins predicted "TMM"

F:361-447/Dominin: Signal InfancyChild #strins predicted /SITS

F:54,145,151/Binding site, carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 CEGGGAEGCAGGTTFTTTTAAGAGAAGGAGTTGTTGTGTA 517 :: [1111] [1:: [1111] [1111] [1111]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 CIIGIACAAAFGACTGTGCAGGCCCGGGGAATACGGAATTGCAGGGAGT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 GTGAGAGGGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 ysAspAsnGlyThrFheThrAlaSerGluAsnHisLeuThrGlnCysLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 AGCTGCTCCAAATGCCGAAAGGAAATGCGGTGGGTGGAGATGTGTTG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 SerCysSerLysCysArgSerGluMetSerGlnValGluIleSerFroCy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 CACAG FGBACCGBBACACCGTGTGTBBCTBCABAAGAACCABTACDBBC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AshClyThrValGlnLeuProCysLeuGlulysGlnAspThrIleCysAs 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 nCysHisSerGlyPhePheLeuArgAspLysGluCysValSerCysValA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 ACTIGITABBAAAGGCCTGGAGCACAAGTTGTGTGTCTAACTAGATTGAG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 snCysLysAsnAla_ Acp^ysLysAsnLeurysProAlaThrSerGl: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 CACCCTCAAAATAATTCGATTTGCTGCTACCAAGTGCCACAAAGGAACCTA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 rodlyAspArgdlutysArgdluSorfou0ysProdlaGlyLysTyrSer 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 HisproClnAshardSorile/ys?ys?hriys?ysHisLysClythrly 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 aLeuLeuValAspValTyrProAlaGlyValHisGlyLeuValLeuHisP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 rLeudisAsnAspCysLeuGlyProGlyLeuAspThrAspCysArgGluC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.670 Gaps: 2
83 412 Percent (dentity: 69,668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 GOTGTTFGGGGAATATACCOCCOCAGGGGTTAFTAFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to JC4302 from 1 to: 461
A; Experimental source: kidney cell line 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 822.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-525-998A-11 x J04302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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                                                                A:Gene: tnfr
C:Superfamily.
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Most term which many of the state of the type I and type 2 murine receptors f A/Peference number: A0254, MUD191246168
A.Accession: B40254
A.Access
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C. Species, Nas muscuius (broase mease)
C. Species, Nas muscuius (broase mease)
C. Pater 30-20: 1920 Health and recrease in the second secon
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A.Tither Nuclearide segrence of the TNF type i temptor from a mouse endothelloma col
A.Reference cumber, 154532, MUIS-94245292
A.Recession: 154532
A.Status: translated trom GB/SMEL/DDBJ
A.Rocecole type: mRNA
A.Residues: 1 454 -- ARIS
A.Cross-references: 0B-LL26349, NID-9430732, RIBN.AAA59361.1, PIB-9430733
A.Cross-references: 0B-LL26349, NID-9430732, RIBN.AAA59361.1, PIB-9430733
P.Rothe, J.G.: Rluethmann, B.: Gentz, R.: Lesslauer, W.: Steinmell, M.
Mol. Immunol, 30, 165-1764, 1993
A.Tithe Generale entained and provide the February contine tomor medicals fact.
A.Reference number: 157826, MUID:93156721
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A Status, Preliminary, translated from GB/EMHE/ANYBU
A.Molecule type: A 1445-454 - 4522
A.Molecule type: 1-393 - 07 | 445-454 - 4522
A.Gross-relengence: UP-M/ref5; NID: 4202100; FIEM.AAA4465.1; FIE: 4202102
C.Comment: This protein is one of two distantly related receptors for both INF-alpha A.Gene: TNFR-2
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A;Accession: $19021
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R;Bebo, B.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
tumer deciresis factor receptor 1 precursor : mouse
                                                                                                         200 ThrangAshAspPheGlnAsp1h1GlyThrThr 210
568 AATGITAAGGGCACTGAGGACTCAGGCACCACA 600
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Immunogenetics 34, 338-340, 1991
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                                                                                                                                                                                                                                                                                                                                                                                            seq_name: pir1:6QMST1
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E)127 167/Samain NOF respitor report homology sNSS.
E)168-2044 Thumsic NOF reseptor report homology sNSS.
E)168-2044 Thumsic normalization regions prodicted AMBN-
E)214-454 Thumsin intracellular metalis predicted AMBN-
E)234-454 Thumsin intracellular metalis predicted simps.
E)54,151,202/Rinding site carbohydrate (ASD) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 isCysLysLysAsnGluGluCysMetLysLeuCysLeuProProLeu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......GATAGTGTGTGTGTGAAGGAAAATATATG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 CACCCTCAAAATAATTGGATTTGGTGCTAGGAAGTGCCACAAAGGAAGCTA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 CTTGTANAATGACTGTCCAGGCCCGGGGAGAGAGAGATATGGGACTGGAGAGAGT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 AGCTIGGTOCAAATGGGAAAGGAAATGGGTGGAGATGTGGAGATCTTGTTG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PACAGIGGAPPGGGAPAPPGIGTGTGPPGGAAGAAGAAPPAGTAPPGGC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 sCinAlaAspLysAspThrValCysCiyCysLysCluAsnCinPhcCinA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 ATTATTGGAGTGAAAAOCTTTTTCACTTCTTCAATTGCAGCCTCTGGCGTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 AATGGGACCGTGCACCTCTCTCCTCCCAGGAGAACAGAACACACTGTGCAC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 CTGCCATGCAGGTTTCTTAGAGAAAAAGGAGTGTGTCTCCTGTAGTA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 ACTOTAAGAAAAGOOTIGGAGIGGAAGTIGTGOOTA...CCCCAGATT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetGlyteuProThrValiroClyteu.culcuScrLeuValiculcuAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGGGCPTCPTGACCTGCTGACCTGCTGCTGCTGCTGGTGGTGGTGCTGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio 4 523 Caps: 2 Percent Similarity: 82.464 Porcon: Identity: 65.351
                                                                                                                                                                                                        Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGA
                                                                                                                                                                                                                                                                                                                                                                                        Align Seq 1, 1 to. 3gMSI1 trun. 1 to. 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 787.00
                                                                                                                                                                                                                                                                                                             alignment_block.
US-09-525 998A 11 x GQMST1
                                                                                                                                                                                alignment_scores:
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RyHimmler, A., Maurer Feay, I.; Kroenke, M., Scheurich, P., Ffizenmaier, K., Tante, M. DNA Cell Biol. 9, 705-715, 1990 A;Title: Molecular cloning and expression of human and rat tumor necrosis factor rece A;Reference number A36555, MHD 91090841 CSCOMMENT. This protein is one of two known receptors for both INF alpha (cachectin) CSCOMMENT. This protein is one of two known receptors for both INF alpha (cachectin) CSCOMMENT. Therefore it cachectin receptor transmembrane protein Cirity Communication, alpha sequence astatus predicted transmembrane protein Cirity Communication and asquence astatus predicted is a sequence as a sequence as a sequence of the cachect cache it is a sequence as a s NyCentains, tymer nucrosis factor binding protein 1 (TNP blocking factor) C.Species: Mattus nervegieus (Norway rat) C.Date. 30 hun-1992 msequence_revision 67 her 1994 #text_change 22-Tun-1999 C.Accession: B46555 212-234/Domain. transmembrane #status predicted <MEAN>
235-461/Domain. intracellalar #status predicted <INT>
54,151,201/Minding site: carbohydrate (Asn) (covalent) #status predicted A;Cross-references: GB:M63122; NID:q207361; P!DN:AAA4225611; PID:q207362 84 ysAsplysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLeu 100 268 AGCTGCTCCAAATGCGAAAGGAAATGGGTCAGGTGGAGGATCTCTTG 317 101 SerCysLysThrCysArgLysGluMetPheGlnValGluIleSerProCy 117 318 CACACTIONARPOGGARPAPOGGTIGTIGTICTAGGARGARGAGGAGTAGFGGG 367 368 ATTALTGGAGLGAAAGCTTTTGGAGTGCTTCAALTGGAGGCTGTGGGCTC 417 134 (1977) London Guthar Bishod Suffsys Malfors Sufficient Action South Control of Sufficient Suffi GATAGTGTGTGTCCCCAAGGAAAATATATC 117 158 TELECTACABETACTORING FOR GRAND GRAND GRAND GRAND GRAND GRAND GRAND THE TRANSPORT OF THE 117 sLysAlaAspMetAspThrValCysGlyCysLysLysAsnGlnPheGlnA 134 17 aLeuLeuMetGlyIleHisProSerGlyValThrGlyLeuValProSerL 34 774.50 | length; 210 4.583 | Gaps: 1 80.476 | Percent Identity: 64.762 51 GOLG FEGLIGEGAATATAGEGEL CAGGGGTTTATTEGA Align seg 1/1 to: GQRTT1 from: 1 to: 461 alignment_block: US-09-525-998A-11 x GQPTT1 A;Molecule type: mRNA A;Residues: 1:461 <HIM> ouality: Percent Similarity: Ratio: A; Accession: B36555 F;212-234/Domain. F;235-461/Domain; alignment_scores:

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seq_documentation block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pirl:GOHUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies. Home sapiens (man)
Cispecies. 4. May 1996 #sequence_revision 24 May 1996 #text_change 17 Mar 2000
Cinate: 24 May 1996 #sequence_revision 24 May 1996 #text_change 17 Mar 2000
Cinatesion: 154182.
Ribaens. M.; Chaltanel, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
Anitic: Construction and evaluation of a hncDNA library of human 12p transcribed sequence number: 154182; MULD:93352381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Map position: 12p13 3-12p13 1
C:Superfamily: tumor necrosis lactor receptor type 1; NGF receptor repeat homology
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                             ::|||||||||||::
184 isCystysAsrGlnGluCysMelLysLeuCysteaProPreValAla 200
418 AAIGGGACCHIGHAPPIPINIONAGAAAAANAAAANAOHIGIGIAN 467
                                                                                                                    468 CIGCCAIGCAGGIIICIFITAAGAAAAAGGAGIGIGIGIGTGTAAGA 517
                                                                                                                                                                              167 nCysHisAlaSlyPhePheLeuSerSlyAsnGluCysThrProCysSerH 184
                                                                                                                                                                                                                                        518 ACTICTAAGAAAACCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 GCCACTGGTGGTGGTGGAGGTGTTGGTGGGAATATACCCCTCAGGGGTTA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor necrosis factor receptor 2 related protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213.50 Length: 214
1.923 Gaps: 11
51 869 Percent Identity: 30.841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Accession: 154182
A:Status, Preliminaly, Manslated How GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                   568 AAIGITAAGGGCACIGAGGACICAGGCACC 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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A:Pesidues: 1-435 <PES>
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Ratio:
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A)Cross-references: GB:M14764; NID:g189204; PRUN:AANE9544.1, PUD:q189205
R)Martho, N. Dierzehend, H.; Earley Jr., G.J.; Schaffrman, G.; Chompson, S.; Grob,
J. Nebrooken, 48, 225–222, 1987
A)Title: Purilication and amino terminal sequencina of toman melanoma nerve growth ta
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AyResidues: 183 per VISA
BySchool A.: Patti, N.: Chao, M.
Mol. Cell. Biol. B. 310-4167, 1988
A.: Lic. A constitution promoter directs expression of the nerve arowth factor recept
AyReterence number: 157638; MUID:89096963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Homo sapiens (man)
Cindre: 21-Mar-1948 #sequence_revision 31 Mar 1968 #iext_change 38 Dec 2000
Cindre: 21-Mar-1948 #sequence_revision 31 Mar 1968 #iext_change 38 Dec 2000
Cindression Dividuals, Actific Buck, Cir.; Schwal, A.; Mougan, C.; Mercer, E.;
Coll 47, 545-554, 1986
Aviitle: Expression and structure of the human NGF receptor.
Aviitle: Expression and structure of the human NGF receptor.
Aviitle: Av
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N.Alternate names: NGF receptor
                                                                                                                                                                                                                                                                                                            103 oCysAspProValMetClyLeuCluciulIeAlaProCysThrScrlysA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 GAAAACQITTITCAGTGCTTCAATTGCAGCCTC.........TGCCTCAA 419
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279 AISPEAAAAAAAAAISSSISAASISSAAAISHITIISMA YAHASAYN 328
                                                                                                                                                                                                                                      329 GGGACACOSIGICISCISCISCANDANDANCANTACOSOCATIALISCASI 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 ysValProCysLysAlaGlyHisPne.. ..GlnABhThrSerSerPro 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 SerAlaAr40ysGluProHisThrAr40ysGluAsc.1Lu3iyLev.
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A)Accession: A60204
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A)Status: prélimmary
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A; Residues: 1-22 < RES
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229 TOCKICACOCCITICACAAANNAANGAGAGAGIGMOTOAGINGGIGGAA 278

71 ysCys...SerArgileArgAspThrValCysAlaThrCysAlaGluAsn

88 ...GATAGTGTGTGT......GATAGGAAAATATATGCAGGCTGAAAA 128

39 GluAsnGlnThrdysArqAspCliGluLysGluTyrTyrGluFroGlnHi 55

22 heGlyteutguAlaAsarGinProGinAlaValProProTyrAlaSer 38

129 TAATITGGATTIGGTGTGGGAAGGGAAGGTAGTTAGTTGTAGTAGTAG 178

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This protein is thought to form a high affinity receptor when it associates withis receptor undergoes both N- and O-linked glycosylation.
                                                                                                                                                                                                                                               CKEYWOLDS: duplication, glycoprotein, heterodimer, monomer, phosphopiotein, receptor, pp.2-2875chaum, siqual sequence #status predicted SNGs |
P.12-2875chaum, siqual sequence #status predicted SNGs |
P.29-2567homain, extracellular #status predicted GEXT; |
P.29-2567homain, extracellular #status predicted GEXT; |
P.32-675chamain, nor proceptor report homology NGS; |
P.567-088.5mmain, NCF receptor report homology NGS; |
P.109-1177homain, NCF receptor repeat homology NGS; |
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C:Superfamily, nerve growth faster resigner; NGE resigner regigt hymology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E)149-189/Thomain NRF ieseptor report hambay NRP
E)197-248/Region: serine/threonine-rich
E)251 272/Domain- transmembrane status prodicted of PRNS
E)273 427/Domain: intra-cliular #status prodicted of NRS
E)273 427/Domain: intra-cliular #status prodicted of NRS
E)60/Ennding site: carbobydrate (Asn) (covalent) #status predicted
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Ratio: 1.921 Caps: 12
Wilarity: 55.670 Percent identity, 31.443
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US-09-525-998A-11 x GQHUN
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                                                                                                        A; Gene: GDB:NGFR
                                                                              C:Genetics:
                                 C:Comment
       C:Comment
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R;Meisis, M.; Timmusk, T.; Allikmeis, P.; Saarma, M.; Persson, H.; Gene 121, 247-254, 198.
A;Tille, Regulatory elements and transcriptional regulation by testosterone and retin A;Reference number: PH1229; MUID:93077038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A criss references of X61269 C. Comment. This receptor is found on sensory and sympathetic neurons, on neuroblastom C. Comment. This receptor is found on sensory and sympathetic neurons, on neuroblastom C. Comment. This receptor is found to term a high-affinity receptor when it associate C. Comment. This protein is thought to torm a high-affinity receptor when it associate
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P.1-29/Fromain: signal sequence #stains predicted >SIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Tille: Gene Fransfer and molecular cloning of the rat nerve growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Speries Partus mervegicus (Norway rat)
C.Bate 10.5rp 1999 #seggenee_revision 10 Smp-1999 #text_change 10-Sep 1999
C.Accession, A26A13, PH1229
F.Padeke, M. T. Miske, F. Hsu, C., Herrenberg L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Superfamily, nerve growth factor receptor; NSF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-425 /PAD>
A;Cross-references: GB:X05137; NID:q56755; PIDN:CAA2R7R3 1; PID:q56756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E)30-425/Product inerve growth factor receptor #status predicted <MATS E;30-251/Demain: extracellular #status predicted <EXTS E;33-66/Domain: NGF receptor repeat homology <NGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1352-273/Domain: transmembrane #status predicted *MEM>
1274-425/Domain: intracellular #status predicted <INT>
(61/Hinding site; carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 GCTGTACCAAGTGCCACAAAGGAACCIACITGTACAAIGACTGTCCAGGC 189
166 oCysThrValCysCluAspithrCluArgClnLeuArgClu^ysThrArgT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 TAGTGTGTGTCCCCAAAGGAAAATATAFCCCTCAAAATAATTCGATTT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 COGGGGGAGGATACGGACTGCAGGGAGTGT GAGAGGGGCTCCTTCAC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 ysCysLysAlaCysAsnLeuGlyGluGlyValAlaGlnProCys...Gly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 sGluThrCysSerThrGlyLeuTyrThrHis.....SerGlyGluC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 GTGCTCCTGCAGCTGTFGGTGGGAATATAGGCGTCAGGGGTTATTGGAGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent identity: 30.208
                                                                                                                                                                                                                                                                                                                                                                             nerve growth factor receptor precursor, low attinity N.Alternate names. NGF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E,68 169/Foundin. NGF receptor repeat homology >NG2> E,110 148/Domain. NGF receptor repeat homology <NG3> E,150 190/Foundin: NGF receptor repeat homology >NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . q ; buon
                                                                                   548 TGTGCCIACCCAGATTGAGAAIGITAAGGGC 579
                                                                                                                                                                  183 rpAlaAspAlaGluCysGluGluIleProGly 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: A26431 from: 1 to: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Reference number: Az6431, MULD:871!5859
A;Accession: A26431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:198-249/Region: serine/threonine-rich
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1.825
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IRS-09-525-998A-11 x A26431
                                                                                                                                                                                                                                                                                                                                          seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-20 <MET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     guality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: FH1229
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60 AlaAsnGlnThrValCysGluProCysl.cuAspAsnValThrPheSe 75	112
237 CGCTTCAGAAAACACACLAGAAAATTEPPPPPPPPPPPPPAAAAAAGGGAA 286	111
rAspValValSerAlathrClupreCystysPreCysThrGluCys	151 TOGGADAADDARGNIATISIACAATOANGIGIGAADDAGGADAAADA 200
ACCACACIOCOCICACIONES O TOTAL ACCACACIONAM (CONTRACTOR CONTRACTOR	
91LeuGlyLeuGliserMetserAlaProCysValGluAlaAspAsp 105 334 ACCGGGGCCTCCAGGAAGAAGAGCAGTAGCGGATTATTCGACTGAAAA 383	201 TACGACTGCACGCACTGTACACACCTTCACCTTCACAAAACC 250 :111
104 AlavalCysArgCys AlatyrClyTyrTyrClsAspClbCl 119 384 CTTTTTCAGEATCAATGAAGCPTGAATGAACATCAATGAAGAAC	251 ACCICAGACACIGOTICAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
:::III :::III :::III :::III :::III :::III :::III :::III :::IIII :::III :::III :::III :::III :::III :::IIII :::III :::IIII :::IIIIII	258 CAGGGGAGATCT::::::0CATAGTGGACGGGAGATGGGGGGGGGGGGGGGGGGGGGG
::: ::	348 CAGGAAGAACCAGTACGGCATTATTGAACCTTTTGCAGTGCT 397 106 SECT ht Giftashirt Pyslediegivski vilhashirt
	TOAALPSCACETSTORTSCAATOSCACESCOATOTISSES TRACSACES SELLE SEL
	AAACAGAACACGIGIGCACGIGCAGGAGGHICTITICTAAGAGAAAA
554 FACCCAGATICAGAGGC 579 184 FACCCAGATICTAGGGC 579 186 SpalaGluCyadluGluIleProdly 194	128
seq_name: pir2:843692	
seq_documentation_block: T2 protein - rabbit fibroma virus C;Species rabbit libroma virus Shope fibroma virus C;Species rabbit libroma virus Shope fibroma virus C;Date, 30 septified assemble leviston of septified attext change 07-May-1999	548 IGCCLACCCCASATUGAGAATGTTAAGGGACTGABGACTCA 591 111 111:: 140CysFroFroRightalycSerAspSerPeroThiglaAraCys 164
C: Accession: H43692 Vipton, C:: Delange, A.M.; McFadden, G.	592 GGGGTAGA 600
A)Tille Tumorispanic poxyituses, genomic organization and DNA sequence of the telomeric A)Reterence number, A43692, MUID:87321103	
Ayardession: Babaya Ayardession: proliminary AyMologule type: PNA	seq_documentation_block: T2 proting
A:Residues: 1-325 <upt> A:Cross-references: GB:M17433 C:Superfamily: myxoma virus T2 protein, NOF receptor repeat homology</upt>	C;Species: myxoma virus C;Date: 31-Dec-1992 #sequence_revision 31-Dec 1992 #text_chadge 16-Jun-1999 C,Assession: A4u566
ED94-147/47main - NaF reagrich repeat haditogy -NGD2 Ej106-147/45mmain - NOF reachthr repeat bamplogy -NCD3	R.Opton, C., Maten, J.L., andreiber, M.; Motadden, G. Virology 184, 370 182, 1991 Allitle: Myxama Virus expresses a secreted protein with homelogy to the tumor necrosi
Lscores: Quality: 190.50 Length: Ratio: 1.832 Gaps:	
	A.C.Sas Terrorities. C.Superfamily: myxema virus 12 protein; AGT receptor repeat homology C.Keywords: diyeoprotein
05-04-77-744A-11 X 443692 Align seq 1/1 'no P43692 (20m : 1 'no 125	Fib6-10/YDOmain: MR receptor repeat homeloay MS2» E)46-14//Comain: MR receptor repeat homeloay MS3 E)46.191.205.238/Endita Sire, Tathoh, dash (Asa) (alent) #status predicted
25 CIGCTGCCACTGCIGCICCIGGAGCTGTIGGIGGAATATACCCCTC 74 ::: :::: :::: ::: :::	alignment_scores: Quality: 187.50 Length: 242
AGGGGTAITGGAGATAGIGTGTGTCCCCAAGGAAAA	1.659 Bercent Identity: 25.
16GlyAspAspValProtyrScrScrAsnClnCtytysCysC 29	alignment_block:

US-09-525-998A-11 x CQV2ML ...

196 LysThrSerGluPheSerValThrLeuAsnHlsThrAspCysAspProVa 212 82 ATTOGAGATAGTGTGTGCCCGAAGGAAAATATATCCACCCTCAAAATA 130 131 ATTICATITICITATOAAGTGAQAAAGGAAOTTAOTTGTAOAATGAO 180 181 TGTCCAGGCCGGGGAAAAAATACGAACTGAAAGGGAAGGGGGCTG 230 231 CTTCACCGCTTCAGAAAACCACTCACACTGGGTCAGGTGGC...TCCA 277 278 AATIGOOGAAAGGAAATIGOGTOAAGTOTOAAATOTOTTOTTTGGAOAGTOAA 327 100 ArgAspArgValCysAspCysSerAlaClyAsnIyrCysLeuLeuLysCl 116 116 y6lmGluGlyCysArgIleCysAlaProLysThrLysCysProAlaGlyT 133 133 yrdlyValSerGlyHidThrArgThrGlyAspValLeuCysThrLysCys 143 364 ... CGGGCATTATTGGAGGGAAAAAAAAAATTTGCCAGGGGGGAATTGGAATTGGGATAT 150 ProArgTyrThrTyrScrAspAlaValSerSerThrGlufhrCysThrSe 166 411 CTGCCTCAATGGG ACCGTGCACCTCTCCTGCCAGAGAAACAGAAACA 457 166 rSerPheAsnTyrIleSerValGluPheAsnLeuTyrProValAsnAspT 183 458 COGREGIOACOTGCCATGCAGGTTTCTTTCTTAAGAGAAAAGGAGTGTGTC 507 ProAsnGluValVal 195 CANTO ACCANGET 548 22 yAlaAspArqGlyLysCysArqGlyAssAspTyr.....GluLysA 36 36 spGlyLeuCysCysThrSerCysProProGlySerTyrAlaSerArgLeu 52 68 rPheThrAlaSerThrAsnHisAlaProAlaCysValSerCysArgGlyA 85 6 Louison equalatyrValAlaCysValTyrSlyClyClyAlaProTyrCL 22 549 GTGCCTACCCAGATTGAGAAATGTTAAGGGCACTGAGGAACTCAGGC 594 40 GIGCICCIGGAACTGTTGCTGCCAAATATACCCTCTCAGGGTT 328 CGGGACACCGTGTGCGCTGCAGGAAGAACCAGTAC Align seq 171 to: GQVZMI, from: 1 to: 326 508 TCCTGTAGTAACTGTAAGAAAAGGCTG 183 hrSerCysThrThrThrAlaGly.

seq_name: pir2:B38634
seq_documentation_block:

seq_documentation_block:

tumor necrosis tactor receptor type 2 precursor - mouse
C:Species: Mus musculus (bouse mouse)
C:Species: Musculus (Bus Mus

A.Residues: 1-474 <LEW>
A:Cross-references: GR M60469; NID:g199827: PIDN:AAA39752.1; PID:g199828
B:Goodwin, B.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, G.L.; Gopeland, N.G.; J. M01 Pell Riol II, 4020-3026, 1991
M01 Pell Riol II, 4020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors 1. A.Reference number: A40254; M01D:91246168 A)Cross references: GB-M60469, NID-9199827; FIEN-AAA39752 1; FID-9199828 R.Kissonerghis, M., Fellowes, R., Feldmann, M., Chernajovsky, Y. submitted to the EMBL Data Library, May 1995 A, Pascription, Characterization of the producer region of the murine p25-PNF receptor A,Reference number: \$54816 A,Accession: \$54816 C)Superfamily, tumor necrosis factor feeeptor type 2, NGF teceptor repeat homology C;Keywords: cytokine receptor, transmembrane protein.

F)1-22/Pomain: signal sequence #status predicted <SIG>
F)23-474/Freduct: tumor peerosis factor receptor type 2 #status predicted <MAI. ACCIOSSITETETETET : IMB.:X87128, NID 9809043, PIDN CAAGOGIR 1, PID 9809044 97 IGICCCCAAGGAAATATATATCCACCTCAAAATAAFICGAITIGCTGTAC 146 147 CAAGTGCCACAAAGGAACCTACTTGTACAATGACTGLCCAGGCCCGGGC 196 GinValGluIl@ArgAlaCysThrLysGlcGlcAsnArgValCysA 120 CGGCATTATTGGAGTGAA 381 120 ladysclualadlyArgTyrCysAlaLcutysTtrHis.....SerCly 134 382 ANOTHTE CASPSTELLIAALISCASSICIONAS TOTOS TOTOS ALCO 135 SerCysArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyVa 151 429 GCACCTCTCCTGC/ASSASAAA/AGAA/ACTGTSTG 7. ACCTGCCATG 475 476 CAGGITICITICINAGAGAAAACGAGIGIGICICCIGIAGIAACIGIAAG 525 197 AGGATACGGAPTGPAGAGAGTGTGAGAGGGGCTPPPTCACACTTFAGAA 246 151 lAlaSerSerArgAlaProAsnGlyAsnValLeuCysLysAlaCysAlaP 168 40 CysGlnIleSerGluGluTyrTyrAspArgLysAlaGlnMetCysCysAl 56 56 aLysCysProProClyGlnTyrValLysHisPheCys...AsnLysThrS 72 181.00 Length: 161 1.946 Gaps: 8 57.764 Percent identity: 31.677 P.166-203/Dommain. NCF receptor repeat homology <NG4> F;40-77/Domain. NGF receptor repeat homology <NG1> F;79-120/Domain. NGF receptor repeat homology <NG2> Align sog 1,/1 to: H38634 from: 1 to: 474 344 GCTGCASSAAGAACCAGTAC US-09-525-998A-11 x B38634 A; Pesidues: 1:474 egges A; Molecule type: DNA A; Residues: 1-22 <KIS> A; Molecule type: mRNA A;Status: preliminary Quality: Percent Similarity: Ration A; Accession: A40254 alignment_scores: alignment_block

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C:Superfamily, fumot necrosis factor fecepter type 2, NGF receptor fepcal homology E:151-188/Nomain: NGF receptor repeat homology <NGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArTitle: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: 148854; MGH::95178848
A;Accession: 148854
                                                                                                                                                                                                                                                             gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Pute: 02 Jul 1996 #sequence_revision 02:Jul:1996 #text_charge 23 Jul 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Cross references: EMBL.X76401; NID-9433830; PIDN.CAA53981 1; PID-9433931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 TGTOCCAAGGAAAAIAIATOCACCICAAAAIAAIIQGAIIIGGIISIAC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 AACCACTCAGACATGCCTCAGATGT...ICCAAAIGACGAAAGGAAAT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 GGGTCAGGTGGAGATFTTFTTTTGGACAGGACCGGACACCGTTGTTGT33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnValGluThrArgAlaCysThrLysGlnGlnAsnArgValCysA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCATIAIIGGAGIGAA 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AACCITITCCAGIGGIICAATIGGAGGCTGGGCICAAIGGG...ACCGT 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429 GGACCTCTCCTGCCAGGAGAAAAAGAAAAGGGTGTGC...ACCTGCCATG 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 CAGGITICITICITAAGAGAAAACGAGIGIGICICCIGIAGIAACIGIAAG 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 CAACTOCCACAAAGGAAGGTAJTTGTAJAATGATGTGAGAGGAGGAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 AGGATACGGACTGCAPAGAGTGTGAGAGAGAGTTTTGACTGGTTGAGAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 erAspThrValCysAlaAspCysGluAlaSerMetTyrThrGlnValTrp 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 CysGlnIleSerGlnGluTyrTyrAspArgLysAlaGlnMetCysCysAl 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 aLysCysProPro4lyGlnTyrValLysHisPheCys . AsnLysThrS 57
                                                                                                                                                                                                                                                                                                                                                                      C;Accession: I48854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57,143 Percent Identity: 31.956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Status: preliminary: translated trom GB/EMRL/PPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
526 AAAAGCCIGGAGIGCAGGAAGIIGIGGGIAACC 558
                                                                      183 ProHisArgileCysSerileLeuAlailePro 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 AAAAGCCTGGAGTGCACGAAGTTGTGCCTACCC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: 148854 from: 1 to: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouality: 176.00
Ratio: 1.913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-525-998A-11 x 148854
                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-459 <RES>
                                                                                                                                                seq_name: pir2:148854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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A.Molecule type: no.tcic acid
A.Residucs: 1-287, 197 -384:
A.Cross-reference: D-M9531; MIN.g1552058, PIDM.AAB08705.1, PH..g1553059, OB.M94126
A.Experimental source: BALB.C. liver
A.Note: sequence extracted from NOBI backbone (NUBIP-120357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Filotres, K.M.; Clark, E.S., A.S., A.S., A.S., A.S., A.S., E.S., E.S., A.S., E.S., E.S., A.S., A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: mRNA
A Residues: 1-365 - 10 K
A Cross-references: 19 MB2111, NID: a1553658
A. Hote. Sequence reliabled in M TEI Lathbare (N TEIN, TELE), N TEIN, TELE)
A. Note: this translation is not autoclated in Gentank entry MISCO40A, release 113.0.
A. Hote: this translation is not autoclated in Gentank entry MISCO40A, release 113.0.
B. Chimaldi I C. Lorres F P. Persk, T.A. (2019, E. Clark, F.A.; R.aard, M., Cack
A. Thite: Genomic structure and chromosomal mapping of the murine CD40 gene.
A. Reference number: A46515, MOID: 97094586
A. Arcession: A46515
                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Mus musculus (house mouse)
C.Date: Le Jun 1994 sceptance_revision 18-Nov 1944 stext_chunge 17-Nov-2000
C.Acression: A444476, A46515
                                                                                                                                                                                                                                                                                                                                                      B cell-associated surface molecule CD40. long splice form - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 AGTOFFACAAAQQAACCTACTTOTAPAAFGAGTGTGFAGFFFFGGGGGAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 GATACGGACTGGAGGAGIGIGAGAGAGGGTQCTICACGGTICAGAAAA 248
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56 LysThrGInCysHisProCysAspSetGlyGliPheSetAlaGlaripas 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 LeuteuThrAisValHis.....teudlyGlnCysVallhrGy 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..... AspGly3lnCysTysAspL 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Comment: For an alternative splice form, see PIR:A46515.
C.Comment: For an alternative splice form, see PIR:A46476.
C.Superfamily: CD27 antigor; NCF receptor repeat homology
C.Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NcF receptor repeat homology (NtF)
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168 ProHisArulleCysSerIleLeuAlallePro 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seq 1/1 to: A46476 from: 1 to: 305
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                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                           seq_name: pir2:A46476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cuality:
Ratio:
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349 AGGAAGAACAAAAACGGGCATTATTGGAATGAAAACCTTTICCAGTGCTT 498

CUCKBY

106 Lysqludlydin HistysThrSerLysAspCysGluAlaCysAl 120	23 yThrAsnSerIleSerGluSerLeuLysLeuArqArqArqYalHisGluI 40
399 CAATIGCAGCCICTGCCICAAIGGGACCGIGCACCTCTCCTGCCAGG 445 iii iii (97TGTCCCCAAGGAAATATATCCACCTCAAAATAATTG 135 111 :::111 11 11 11 11 11 1
446 AGAACAGACCGTGTGC ACTGCCATGCTGTTCTTAGA 492 	136 ATTGATGATAGAGAGAGAGAAAQCIACTTGTACAAGACTGACTGTCC 185
493 GAAAAAC GAGTGTGTGTGTAATRITAA3 . AA 527 	186 AbbrichebbinatalArbinataria/BSSASFCHGARGA GATTCTIGA 235 H
528 AAGCCBGAATTGGAQGAAGTTGTGAGAATTGAGAATGTTAAGG 577 - - - - -	236 GOOTHAGAAAAQOTGAGACAGTGCOTGCTGCTGCAAAGC 282 GOOTHAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
578 GCATTGAGGACTCA 591 :::::::: 78 iyThtScrGlnTht 182	283 (GAAAGGAAATGGTTAGGAGATCTCTTCTTGTAGGACGGGA 332
seq_name: pir2:A46484	333 CACCHTATATAAATAAAAAAAAAAAAAAAAAAAAAAAAA
aportosis-mediating membrane associated polypeptide Fas · mouse c.species: Mus musculus (house mouse) c.bate: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C.Accession: A46484; A47254	383 ACCTITITION OF THE ACTION
R:Watanate-Fukumaga, R.; Brannan, C.I.; ILOh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J. Immuncl. 146, 1274-1279, 1992. A; Immuncl. 146, 1274-1279, 1992. A; Fitle: The CDNA structure, expression, and chromosomal assignment of the mouse Fas and A; Reference number: A46484; MTID-92148151	
A;Accession: Atoaest A;Status: preliminary A;Molecule (ype: mRNA	seq_name: pir2:D72175
A)Residues: 1-327 <wat> A;Crcss.references: CR_M83649, N;D,4193225, PIRM.AAA37593.1, PID.4193226 A;Experimental source: BAM3_macrophage cell line</wat>	seq_documentation_block: G2R protein variois minor virus (strain Garcia 1966) C,Species, variols minor virus
Ajmoto: Sequence extracted from MFR Packhoun. (N°3'N'8'N'8'N'8'N'8'N'9') R:Adachi, M.; Watanabe-Fukunaqa, R.; Naqata, S. R:Adachi, M.; Watanabe-Fukunaqa, R.; Naqata, S. R:Occ. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993 A:Title: Aberrant transcription caused by the insertion of an early transmosable element	C. Atternoon 1944 #Sergarian Fernanda 24 Rev 1999 #text_change 26 Jan 2000 C.Accession: D72175 Rishchelkunov, S.N.; Tothmenia, A.V.; Gaterev, V.V.; Safronov, F.F.; Massand, R.F.; Loshmitted to Cambana March 1008
A;Poforono number: A47254; Millo:93189576 A;Accession: A47254 A;Status: preliminary	Appendiction, watering, main in the complete coding sequence of DNA of alastrim variola mi Appendiction, Analysis of the complete coding sequence of DNA of alastrim variola mi Appendict D72175
A.Molecule type: nucleic acid A.Besidues: 1-96 :ADA> A.Cross-reterences: CB:S564an: Nib-q204505: PIDN-AAR35700 1: PID-g208506	A.Status: preliminary A.Molecule type: DNA A Residuce 1 349 : SIF.
AsExperimental source: MRL hpr/lpr AsNote, sequence extracted from MTRL backbear (MTRLN-126856, MTRLN-126853, MTHLN-12685), C.Superfamily: NGF receptor repeat homology	A;Cross-references, GR:Y16780; NID:95830555; PIDN:CAB54798.1; PID:95830759 A:Experimental source, strain Garcia-1966 C;Genetics:
C:Keywords: transmembrane protein E:44-79/Tomain	AyGene: G2R C;Saperfamily: myxoma virus T2 protein; NGF receptor repeat homology
alignment_scores: Quality: 169.50 Length: 161 Ratio: 2.093 Gaps: 6 Percent Similarity: 50.311 Percent Identity: 27.950	alignment_scores: Ouality: 166.50
A46484	alignment_block: US-09-525-998A-11 x D72175
1	Align seg 1/1 to: D72175 from: 1 to: 349
	97 TGTGGGGAAGGAAATAIAGGAGGGGAAAIAAIIGGALLIGGTGTAC 146
7 VALUEUT OLGENAALDE MATEUR OF THE CONTROLL OF THE CONTROL O	147 CAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGGGGGGG

45 uSerCysProProGlyThrTytAlaSerArgLeuCysAspSerLysT 61	
197 AGGATACGANTG-CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	44 üSerCysPr 197 maaminee
61 hrAsnThrGlnCySThrProCySGlySerGlyThrPheThrSerArgAsn 77	: : : :
247 AACCACTGCTCAGACTGCTCAGCTGCTCCAAATGCCGAAAGGAAAT 293 	247 AACCACCTC
294 GARTORARTAROLOTOTORANARARARARARARARARARARARARARARARARARAR	
344 GCTGCAGGAAGCAGIACCGGCAIIAIIGGAGTGAAAACCIIIIICCAG 393 11	92 .ASECINVA 344 GCTGLAGGA
394 IGCTIC	394 100110
429 GCACCTCLCCTGCCTGCAGAACACACACTGTGTGCACACACACACACA	115 CysLeuLeu 429 GCACCYCTC
GITICITICIAAGAGAAAAGGATGTCTCC TGTAGTAAV 	131
520 TGT AAGAAAAGCTGGAGTGCACGAAGTTGTGCT 554	474 161 11
555 ACCCCAGAIIGAGAAI 570 	152 Cys 152
seq_name: pir2:T28623	
seq_documentation_block: hypothetical protein G2R - variola major virus C:Species: variola major virus C:Date: 22 Oct 1999 #sequensc_revision 22-Oct 1999 #text_change 21-Jui 2000	
Rimanessand, 1200-1200-120, J.J.; Liu, I. J.; Qi, J.; Utterback, T.P.; Knight, J.C.; Aubin Rimansund, BS.; 748-751, 1993 A:Ittle: Potential virulence determinants in terminal regions of variola smallpox virus A:Reference number, 220488; MUID:94088747	
Arcression: 128b23 Arcression: 128b23 A:Molecule Type: DNA	
A:Residues: 1-348 <mas> A:Cross-references: PMB::122579; NID:#£23595; PIDN:AAA£9933.1; PID:#439102 A:Experimental source, strain Bangladesh 1975 C:Superfamily: myxoma virus 12 protein: NOF receptor repeat homology</mas>	
alignment_scores:	
alignment_block: US-09-525-998A-11 x T28623	
Align seg 1/1 to: [28623 from: 1 to: 348	
97 TGTCCCCAAGGAAAAIAIGCACCCCCAAAATAAITGGAITIGCTGFAC 146	
147 CARGIGOCACAAAGGAACCTACTIGTACAATGACTGTCCAGGCCCGGGGC 196	

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44 uSerCystroProdigith[11]

45 uSerCystroProdigith[11]

46 uSerCystroProdigith[12]

46 uSerCystroProdigith[13]

47 Ascaltacarded and prodyschyllerith[1]

48 and prodigith[13]

49 dodicacarded and recovered and re
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